

RAW SEQUENCE LISTING

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Application Serial Number: 10/534583
Source: PCT
Date Processed by STIC: 5/19/15

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PCT

RAW SEQUENCE LISTING

DATE: 05/19/2005

PATENT APPLICATION: US/10/534,583

TIME: 10:23:30

Input Set : A:\235670.ST25 - US Sequence Listing.txt

Output Set: N:\CRF4\05182005\J534583.raw

3 <110> APPLICANT: KISHIMOTO, Takahide
 4 SOGABE, Atsushi
 5 OKA, Masanori
 7 <120> TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASE, PROCESS FOR PRODUCING THE SAME

AND

8 REAGENT COMPOSITION USING THE SAME
 10 <130> FILE REFERENCE: 235670
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/534,583
 C--> 12 <141> CURRENT FILING DATE: 2005-05-11
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/014423
 13 <151> PRIOR FILING DATE: 2003-11-13
 15 <150> PRIOR APPLICATION NUMBER: JP2002-329427
 16 <151> PRIOR FILING DATE: 2002-11-13
 18 <150> PRIOR APPLICATION NUMBER: JP2002-329428
 19 <151> PRIOR FILING DATE: 2002-11-13
 21 <150> PRIOR APPLICATION NUMBER: JP2003-33641
 22 <151> PRIOR FILING DATE: 2003-02-12
 25 <160> NUMBER OF SEQ ID NOS: 14
 27 <170> SOFTWARE: PatentIn version 3.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 389
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Arthrobacter SP. TE1826
 34 <400> SEQUENCE: 1

36	Met	Ser	Ile	Lys	Lys	Asp	Tyr	Asp	Val	Ile	Val	Val	Gly	Ala	Gly	Ser
37	1			5						10					15	
40	Met	Gly	Met	Ala	Ala	Gly	Tyr	Tyr	Leu	Ser	Lys	Gln	Gly	Val	Lys	Thr
41				20					25					30		
44	Leu	Leu	Val	Asp	Ser	Phe	His	Pro	Pro	His	Thr	Asn	Gly	Ser	His	His
45			35					40					45			
48	Gly	Asp	Thr	Arg	Ile	Ile	Arg	His	Ala	Tyr	Gly	Glu	Gly	Arg	Glu	Tyr
49		50					55					60				
52	Val	Pro	Phe	Ala	Leu	Arg	Ala	Gln	Glu	Leu	Trp	Tyr	Glu	Leu	Glu	Lys
53	65					70				75					80	
56	Glu	Thr	His	His	Lys	Ile	Phe	Thr	Lys	Thr	Gly	Val	Leu	Val	Phe	Gly
57					85					90					95	
60	Pro	Lys	Gly	Glu	Ala	Pro	Phe	Val	Ala	Glu	Thr	Met	Glu	Ala	Ala	Lys
61				100					105					110		
64	Glu	His	Ser	Leu	Asp	Val	Asp	Leu	Leu	Glu	Gly	Ser	Glu	Ile	Asn	Lys
65			115					120					125			
68	Arg	Trp	Pro	Gly	Val	Thr	Val	Pro	Glu	Asn	Tyr	Asn	Ala	Ile	Phe	Glu
69		130					135					140				
72	Lys	Asn	Ser	Gly	Val	Leu	Phe	Ser	Glu	Asn	Cys	Ile	Arg	Ala	Tyr	Arg
73	145					150					155				160	

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76 Glu Leu Ala Glu Ala Asn Gly Ala Lys Val Leu Thr Tyr Thr Pro Val
77              165              170              175
80 Glu Asp Phe Glu Ile Ala Glu Asp Phe Val Lys Ile Gln Thr Ala Tyr
81              180              185              190
84 Gly Ser Phe Thr Ala Ser Lys Leu Ile Val Ser Met Gly Ala Trp Asn
85              195              200              205
88 Ser Lys Leu Leu Ser Lys Leu Asn Ile Glu Ile Pro Leu Gln Pro Tyr
89              210              215              220
92 Arg Gln Val Val Gly Phe Phe Glu Cys Asp Glu Lys Lys Tyr Ser Asn
93 225              230              235              240
96 Thr His Gly Tyr Pro Ala Phe Met Val Glu Val Pro Thr Gly Ile Tyr
97              245              250              255
100 Tyr Gly Phe Pro Ser Phe Gly Gly Cys Gly Leu Lys Ile Gly Tyr His
101              260              265              270
104 Thr Tyr Gly Gln Lys Ile Asp Pro Asp Thr Ile Asn Arg Glu Phe Gly
105              275              280              285
108 Ile Tyr Pro Glu Asp Glu Gly Asn Ile Arg Lys Phe Leu Glu Thr Tyr
109              290              295              300
112 Met Pro Gly Ala Thr Gly Glu Leu Lys Ser Gly Ala Val Cys Met Tyr
113 305              310              315              320
116 Thr Lys Thr Pro Asp Glu His Phe Val Ile Asp Leu His Pro Gln Phe
117              325              330              335
120 Ser Asn Val Ala Ile Ala Ala Gly Phe Ser Gly His Gly Phe Lys Phe
121              340              345              350
124 Ser Ser Val Val Gly Glu Thr Leu Ser Gln Leu Ala Val Thr Gly Lys
125              355              360              365
128 Thr Glu His Asp Ile Ser Ile Phe Ser Ile Asn Arg Pro Ala Leu Lys
129              370              375              380
132 Gln Lys Glu Thr Ile
133 385

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136 <210> SEQ ID NO: 2
137 <211> LENGTH: 1167
138 <212> TYPE: DNA
139 <213> ORGANISM: Arthrobacter SP. TE1826
141 <220> FEATURE:
142 <221> NAME/KEY: CDS
143 <222> LOCATION: (1)..(1167)
144 <223> OTHER INFORMATION:

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W--> 146 <400> 2

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147 atg agt att aaa aaa gat tat gat gta att gtg gtt ggc gct ggt tcc      48
148 Met Ser Ile Lys Lys Asp Tyr Asp Val Ile Val Val Gly Ala Gly Ser
149 1              5              10              15
151 atg gga atg gca gct ggg tac tat ctg tct aaa caa ggt gtt aaa aca      96
152 Met Gly Met Ala Ala Gly Tyr Tyr Leu Ser Lys Gln Gly Val Lys Thr
153              20              25              30
155 cta ttg gta gat tca ttt cat cct ccc cat aca aat ggc agc cat cat      144
156 Leu Leu Val Asp Ser Phe His Pro Pro His Thr Asn Gly Ser His His
157              35              40              45
159 ggc gat aca cgg atc att cgt cac gca tat ggc gaa gga aga gag tat      192

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160	Gly	Asp	Thr	Arg	Ile	Ile	Arg	His	Ala	Tyr	Gly	Glu	Gly	Arg	Glu	Tyr	
161		50					55				60						
163	gta	ccg	ttt	gcc	ttg	aga	gca	caa	gag	tta	tgg	tat	gaa	tta	gaa	aag	240
164	Val	Pro	Phe	Ala	Leu	Arg	Ala	Gln	Glu	Leu	Trp	Tyr	Glu	Leu	Glu	Lys	
165	65				70				75				80				
167	gag	act	cat	cat	aaa	ata	ttt	aca	aaa	aca	ggt	gta	ctc	gtt	ttt	ggt	288
168	Glu	Thr	His	His	Lys	Ile	Phe	Thr	Lys	Thr	Gly	Val	Leu	Val	Phe	Gly	
169				85					90				95				
171	cct	aaa	gga	gaa	gct	cct	ttc	gtt	gcc	gaa	aca	atg	gaa	gcc	gca	aag	336
172	Pro	Lys	Gly	Glu	Ala	Pro	Phe	Val	Ala	Glu	Thr	Met	Glu	Ala	Ala	Lys	
173			100						105				110				
175	gaa	cat	tca	tta	gat	gtt	gat	tta	cta	gaa	gga	agt	gaa	ata	aat	aag	384
176	Glu	His	Ser	Leu	Asp	Val	Asp	Leu	Leu	Glu	Gly	Ser	Glu	Ile	Asn	Lys	
177			115					120					125				
179	cgt	tgg	cca	ggt	gta	acg	gtt	cct	gag	aat	tat	aat	gct	att	ttt	gaa	432
180	Arg	Trp	Pro	Gly	Val	Thr	Val	Pro	Glu	Asn	Tyr	Asn	Ala	Ile	Phe	Glu	
181		130					135						140				
183	aaa	aat	tct	ggt	gtc	tta	ttt	agt	gaa	aat	tgt	att	cgc	gct	tac	cgt	480
184	Lys	Asn	Ser	Gly	Val	Leu	Phe	Ser	Glu	Asn	Cys	Ile	Arg	Ala	Tyr	Arg	
185	145				150				155				160				
187	gaa	ttg	gcg	gaa	gca	aat	ggt	gcg	aaa	gtt	cta	acg	tac	aca	ccc	gtt	528
188	Glu	Leu	Ala	Glu	Ala	Asn	Gly	Ala	Lys	Val	Leu	Thr	Tyr	Thr	Pro	Val	
189				165					170				175				
191	gaa	gat	ttc	gag	att	gcc	gag	gac	ttc	gtc	aaa	atc	caa	acc	gcc	tat	576
192	Glu	Asp	Phe	Glu	Ile	Ala	Glu	Asp	Phe	Val	Lys	Ile	Gln	Thr	Ala	Tyr	
193			180						185				190				
195	ggc	tcc	ttt	aca	gcc	agt	aaa	tta	att	gtt	agc	atg	ggc	gct	tgg	aat	624
196	Gly	Ser	Phe	Thr	Ala	Ser	Lys	Leu	Ile	Val	Ser	Met	Gly	Ala	Trp	Asn	
197			195				200						205				
199	agc	aaa	ctg	cta	tca	aaa	tta	aat	att	gaa	atc	cca	ttg	cag	cca	tac	672
200	Ser	Lys	Leu	Leu	Ser	Lys	Leu	Asn	Ile	Glu	Ile	Pro	Leu	Gln	Pro	Tyr	
201		210					215						220				
203	cgt	caa	gtt	gtc	gga	ttc	ttc	gaa	tgt	gat	gaa	aaa	aaa	tat	agc	aat	720
204	Arg	Gln	Val	Val	Gly	Phe	Phe	Glu	Cys	Asp	Glu	Lys	Lys	Tyr	Ser	Asn	
205	225				230				235				240				
207	aca	cat	ggt	tat	ccg	gcg	ttc	atg	gtc	gaa	gtc	cca	act	ggc	atc	tat	768
208	Thr	His	Gly	Tyr	Pro	Ala	Phe	Met	Val	Glu	Val	Pro	Thr	Gly	Ile	Tyr	
209				245					250				255				
211	tac	gga	ttt	cca	agc	ttc	ggc	ggc	tgc	ggc	ttg	aaa	ata	ggc	tat	cat	816
212	Tyr	Gly	Phe	Pro	Ser	Phe	Gly	Gly	Cys	Gly	Leu	Lys	Ile	Gly	Tyr	His	
213			260						265				270				
215	acg	tat	ggt	caa	aaa	atc	gat	cca	gat	acg	att	aat	cgt	gaa	ttt	ggt	864
216	Thr	Tyr	Gly	Gln	Lys	Ile	Asp	Pro	Asp	Thr	Ile	Asn	Arg	Glu	Phe	Gly	
217			275					280					285				
219	att	tac	ccg	gag	gat	gaa	ggg	aat	att	cgc	aaa	ttc	ctg	gaa	aca	tat	912
220	Ile	Tyr	Pro	Glu	Asp	Glu	Gly	Asn	Ile	Arg	Lys	Phe	Leu	Glu	Thr	Tyr	
221		290					295						300				
223	atg	ccg	gga	gca	acc	ggc	gaa	tta	aaa	agt	ggg	gca	gtt	tgc	atg	tac	960
224	Met	Pro	Gly	Ala	Thr	Gly	Glu	Leu	Lys	Ser	Gly	Ala	Val	Cys	Met	Tyr	

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225 305          310          315          320
227 aca aaa aca cct gat gag cat ttc gtg att gat tta cat cct caa ttc      1008
228 Thr Lys Thr Pro Asp Glu His Phe Val Ile Asp Leu His Pro Gln Phe
229          325          330          335
231 tcg aat gtc gcg att gca gcc gga ttc tcc gga cat ggg ttt aaa ttc      1056
232 Ser Asn Val Ala Ile Ala Ala Gly Phe Ser Gly His Gly Phe Lys Phe
233          340          345          350
235 tca agc gta gtt ggt gaa aca tta agt caa tta gct gta acc ggt aaa      1104
236 Ser Ser Val Val Gly Glu Thr Leu Ser Gln Leu Ala Val Thr Gly Lys
237          355          360          365
239 aca gaa cac gat att tcc atc ttt tca atc aat cgc cct gct tta aaa      1152
240 Thr Glu His Asp Ile Ser Ile Phe Ser Ile Asn Arg Pro Ala Leu Lys
241          370          375          380
243 caa aaa gaa acg att      1167
244 Gln Lys Glu Thr Ile
245 385
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 38
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
256 <400> SEQUENCE: 3
257 gactcatcat aaaatattta caagaacagg tgtactcg      38
260 <210> SEQ ID NO: 4
261 <211> LENGTH: 36
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
268 <400> SEQUENCE: 4
269 gtgtcttatt tagtgaaaat attattcgcg cttacc      36
272 <210> SEQ ID NO: 5
273 <211> LENGTH: 36
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
280 <400> SEQUENCE: 5
281 gaattggcgg aagcaaaagg tgcgaaagtt ctaacg      36
284 <210> SEQ ID NO: 6
285 <211> LENGTH: 38
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
292 <400> SEQUENCE: 6
293 gccagtaaata taattggttag cgcggggcgct tggaatag      38
296 <210> SEQ ID NO: 7

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297 <211> LENGTH: 38
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
304 <400> SEQUENCE: 7
305 gaatagcaaa ctgctaccaa aattaaatat tgaaatcc 38
308 <210> SEQ ID NO: 8
309 <211> LENGTH: 36
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial Sequence
313 <220> FEATURE:
314 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
316 <400> SEQUENCE: 8
317 gtcggattct tcgaaagcga tgaaaaaaaa tatagc 36
320 <210> SEQ ID NO: 9
321 <211> LENGTH: 38
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
328 <400> SEQUENCE: 9
329 gtgatgaaaa aaaatatagc tatacacatg gttatccg 38
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333 <211> LENGTH: 33
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
340 <400> SEQUENCE: 10
341 ccggcggttca tgggccaggt cccaactggc atc 33
344 <210> SEQ ID NO: 11
345 <211> LENGTH: 37
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial Sequence
349 <220> FEATURE:
350 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
352 <400> SEQUENCE: 11
353 gaaacattaa gtcaattagt tgtaaccggt aaaacag 37
356 <210> SEQ ID NO: 12
357 <211> LENGTH: 36
358 <212> TYPE: DNA
359 <213> ORGANISM: Artificial Sequence
361 <220> FEATURE:
362 <223> OTHER INFORMATION: Arthrobacter SP. TE1826
364 <400> SEQUENCE: 12
365 caaaaacagg tgtactcggg tttggtccta aaggag 36
368 <210> SEQ ID NO: 13
369 <211> LENGTH: 37

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VERIFICATION SUMMARY

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Input Set : A:\235670.ST25 - US Sequence Listing.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:146 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:144